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Gendore version 5.1.3
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OM protein - protein search, using sw model

January 16 2003, 16 39-12 ; search time 7 2857) seconds (without alignments) 28.464 Million cell updates/see Kun on:

ปร-กจ-856-กี7ก-18 24 1 KEELM 5 Title: Perfect score: sednence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters.

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Tomb J. P., White o., Kerlavage A.R., Clayton R.A., Sutton 6.G.,
Tomb J. P., White o., Kerlavage A.R., Clayton R.A., Sutton 6.G.,
Fleischmann R.D., Keltchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
Relson K., Ouackenbush J., Zhou L., Kirkness E.F., Peterson S.,
Loftus H., Richardson D., Dodson R., Khalak H.G., Glodek A.,
Mercanov K., Fitzderald L.M., Lee N., Adams M.D., Hickoy E.K.,
Berg D.E., Gorayge T.B., Therback T.R., Peterson J.D., Kelley J.M.,
Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                       Alm K.A., Ling L.-S.L., Moir D.I., King H.L., Brown E.D., Doig P.C., Smith D.W., Noonan H., Guild H.C., delonge B.L., Carnel G., Immino P.J., Carnso A., Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genomic sequence comparison of two unrelated isolates of the human
                                                                                 Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The complete genome sequence of the qustric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE LIOP FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NATURE 388:539-547(1997).
-!- SIMILARITY: BELONGS TO THE LIDP FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 24; DB 1; Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164 AA; 18573 MW; E307C2448B5F17F6 CRC64;
                                          Helicobacter pylori J99 (Campylobacter pylori J99).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or NOV-1997 (Rel. 35, Last, enquence update).
16-OCT-2001 (Rel. 40, Last, annotation update).
508 Thosenal protein L10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Holicobactor pylori (Campylobactor pylori).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001790; Ribosomal_L10.
InterPro; IPR002364; Ribosomal_L10eub.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ribosomal protein; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ptam; PF00466; Ribosomal_L10; 1.
PROSITE: PS01109; RIBOSOMAL_L10; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P.R.T.;
                                                                                                                                                                                                                                                                                 MEDLINE-99120557; PubMed 9923682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE001540; AAD06701.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.
Hes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          SPONENCE FROM N A
                                                                                                                                                             NCB1_Tax1D-85963;
RPLJ OR JHP1123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 KEELM 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPL, OR HP1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ] KFFTM 5
                                                                                                                       Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RL10_HELPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venter J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P56036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CREE CARRES CON CORRES CON CONTRACTOR CON CONTRACTOR CON CONTRACTOR CONTRACTO
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the EUROPEAN BOINFORMATICS INSTITUTE. There are no restrictions on its use by ron-profit institutes as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Hioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the Buropean Biointormatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and Institutions as long as its content is in no way modified and this statement is not removed. Usage by and for connectial cutties regulies a license alreament (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      actin-regulatory proteins exhibit high structural homology.";
Biochemistry 29:7420-7425(1990).
-!- FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERS ACTIN FILAMENTS (F-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves, Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE 91027755, PubMed-1699599; Abha H. Janamoto K., Obinata T.; Sanamoto K., Chinata T.; Sanamoto K., Chinata T.; Sanamoto No. Sanamoto M. Sequence of charten and cotiling of embryonic chicken skeletal muscle: two functionally distinct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Nucleotide sequence and expression of a cDNA encoding chick brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INDEPENDENT MANNER.
-:- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
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o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 24; DB 1; Length 164; 100.0%; Pred. No. 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0) Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 101-111 AND 116-134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9915415D78AF5D97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adams M.E., Minamide L.S., Duester G., Bamburg J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1990 (Fel. 16, last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Destrin (Actin-depolymerizing factor) (ADF).
DSIN OR DSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0, Mismatches
                                                                                                                                                                                                                                                            or send an email to licensesish-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002363; Ribosomal_L10eub.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribosomal protein; Complete proteome
SEQUENCE: 164 AA; 18605 MW; 99154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00466; Ribosomal_L10; 1.
PROSITE; PS01109; RIBOSOMAL_L10; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPP001790; Pibosomal_L10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-91027754; PubMed-2223773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                actin depolymerizing factor.";
Biochemis⁺r; 29-7414-7420(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1990 (Rel. 16, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                         EMBL; AE000626; AAD08246.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5, Conscivative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Skeletal muscle;
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A MEDINE-1584 49, PubMoor 1780052,

A Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,

BA Tones M., Staveldes G., Alacida J.P., Rabbage A.K., Beare D.M.,

RA Basiley J., Barlow K.E., Bates K.N., Beare L.M., Beare D.M.,

RA Basiley J.S., Bild C.E., Giakey S.E., Blidgeman A.M., Brown A.J.,

RA Buck D., Burrill W.D., Clark G., Clark L.M., Clark S.Y., Clee C.M.,

RA Clegg S., Cobley V.E., Collier R.E., Comnor R.F., Corty N.R.,

RA Culson A., Coville G.T., Deadman R., Dhami P.D., Dunn M.,

RA Culson A., Coville G.T., Deadman R., Dhami P.D., Dunn M.,

RA Burkle R., Hunt A.R., Hunt S.R., Holden L., Garrer P.,

RA Hammond S., Harley J.L., Heath P.D., Ho.S., Holden J.I., Ghinson D.,

RA Harley J.L., Martin S.L., McConsorlie J. T., McCort S.R., Johnson D.,

RA Marsh V.L., Martin S.L., McConsorlie J.T., Norder S.N., Honsey H.,

RA Milne S.A., Mistry D., McConsorlie J.T., Norder S., Mistry D., Moore M.J.F., Studen S.R., Plunb R.M., Ramsay H.,

RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Showkou P., Sins, S.,

RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Showkou R.,

RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Showkou R.,

RA Tacey A., Tromans A. Vandin M., Wallis T.M.,

Whittelead S.L., Whittaker P., Whilley D.L., Williams L., Williams S.A.,

Wilming L., Wray P.W., Hubbard T., Durbin R.M., Hontpe A.,

Wilming L., Wray P.W., Hubbard T., Durbin R.M., Hontpe Y.,

Whitting L., Wray P.W., Hubbard T., Durbin R.M., Hontpe Y.,

Williams B. Williams L., Whitting D.L., Williams L., Williams S.A.,

Wilming L., Wray P.W., Hubbard T., Durbin R.M., Hontpe Y.,

Whitting L., Wray P.W., Hubbard T., Durbin R.M., Hontpe Y.,

Whitting L., Wray P.W., Hubbard T., Durbin R.M., Hontpe S.,
                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                             NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metázóa, Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria, Primates; Catarrhini, Hominidac, Homó.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES=Human; IISSUE-Brain;
MFDLINE=940n20n9; pubMed-8399167;
Hawkins M., Pope B., Maciver S K , Weeds A G ;
Hawkins M., Maciver S K , Weeds A G ;
destruction of actin fizing factor mediates a pH-sensitive
destruction of actin fizing factor.;
Biochemistry 32.9985-9993(1993)
                                                                                                                                                                                                                           100 0%, Shere 24, DR 1, Length 165, 100.0%, Pred. No. 54,
                                                                                                                                                                                                                                                             0; indels
                                                                                                                                                                                ACTIN-BINDING (POTENTIAL).
7FND20ND24519R629 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        DESI_HUMAN STANDARD; PRT; 165 AA. P18.282.
P18.282.
DI.NOV-1990 (Rel. 16, Last sequence update)
15-JUN-2002 (Rel. 14, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
DSTN OR DSN OR ACTOP.
                                                                                                                                                                                                                                     100.0%, Pred. no.
                                                                                                                           PROSITE: PS00325; ACTIN_DEPOLYMERIZING: 1. Actin-binding.
                                              InterPro: IPR002108: Actbind_cofln.
                                                                              PRINTS; PROGODA; COFFLIN
Probom; PD002129: Actbind_cofin: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES-Human;
MEDLINE-21638749; PubMed-11780052,
                                                           PF00241, colilin_ADF, 1.
                                                                                                                                                                                          TAS AA; 18522 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human), and
                                                                                                                                                                                                                                            Local Similarity 100.
hes 5; Conservative
                                                                                                                                                               34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606, 9823;
               PIR; A35703; A35703.
HSSP: P18282: 1AK6.
                                                                                                               ADF;
PIR; A35702; A35702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa (Pig).
                                                                                                                                                             30
                                                                                                                                                                            106
                                                                                                               SMART; SM00102;
                                                                                                                                                                                                                                                                                                                            96 KEELM 100
                                                                                                                                                                                                                                                                                            1 KEELM 5
                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                              Query Match
                                                                                                                                                               DOMAIN
                                                                                                                                                                                DOMA I N
                                                                 Ptam:
                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBLO outstainonthe EMBLO outstainonthe EMBLO outstained the EMBLO outstained is the are not or estrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ! FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN, SEVERS ACTIN FILAMENTS (F-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Actin-binding; 3D-structure.
DOMAIN 30 34 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Tertiary structure of destrin and structural similarity between two
"The DNA sequence and comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                         "Destrin, a mammarian actic depolymenting protein, is closely
related to colliin. Cloning and expression of porcine brain destrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -! - SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTIN) AND BINDS TO ACTIN MONOMERS (G-ACTIN). ACTS IN A PH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INDEPÉNDENT MANNER.
-!- IISSUE SPECIFICITY: WIDELY DISIKIBULED IN VAKIOUS TISSUES.
                                                                                                                                                                                                                                                                                                                                          Moriyana K., Nishila F., Yanazawa N., Sakai H., Matsumoto S.,
Iida K., Yahara I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hatanaka H., Ogura K., Moriyama K., Ichikawa S., Yahara I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lum ma, Samre 24; OB 1; Length 165; 100.0%; Pred. No. 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                        Strausberg R.;
Submitted (JUN 2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 ACTIN-BINDING (POTENTIAL).
1850A MW: 8868A2167924100E CRC64;
                                                                                                                                                                                                                                              SEQUENTE FROM N.A., AND SEQUENCE OF 53-69 AND 96-112.
SPECIES-Plg; TISSUE-Brain;
MIDLINE 90202824; PubMed-2156828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 AA.
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PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       actin-regulating protein families.";
cell 85:1047-1055(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro. IPE692108, Actbind_cofin.
Pfam: PF00241; colllin_ADF; 1.
PKINIS: PRO006; GOFILIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pretom; PP002129; Actbind_cofin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hiol. Chem. 265:5768-5773(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-96270507; PubMed-8674111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ċ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; S65738; AAB28361.1; -.
                                                                                                                          SPECIES-Human: Tissue-Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D90953; BAA14105.1;
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                             Nature 414 865-871(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDB; 1AK6; 12-NOV-97.
PDB; 1AK7; 15-OCT-97.
Genew; HGNC:15750; DSTN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A35179; A35179.
PIR; A54184; A54184.
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                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRUCTURE BY NMR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 KEELM 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES-Pig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inagaki F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPSI_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA."
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VA34_VACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.sib.ch/announce/or send an email to licensewisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seki N., Hattori A., Hayashi A., Kozuma S., Muramatsu M., Saito T.; "Mouse actin depolymerizing factor sid23.";
Submitted (MAR-1990) to the EMBL/GenBank/DobJ databases.
-!- FUNCTION-ACTIN-DEPOLYMERIZIN; PROTEIN. SEVERS ACTIN FILAMENTS (F-ACTIN) AND BINDS TO ACTIN MONOMERS (G-ACTIN). ACTS IN A PHINDEPENDENT MANNER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
ACTIN-BINDING (POTENTIAL).
42RP079R4C9R3667 CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CENTER STRUCTURE AND FUNCTION. -1. SUBCELLITAR FOCATION: CENTROSOME OF INTERPRESSE AND MIDORIC CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhu J. K., Bressan R.A., Hasegawa P.M.;
"An Atriplex nummularia cDNA With sequence relatedness to the algal
                                                                                                                                                      Mus musculus (Mouse).
Eukaryota, Motaroa, Glordata, Craniata, Vertebiata, Euteleostomi;
Mammalia; Eutheria, Rodentia, Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bokaryota: Viridiplantae: Streptophyta: Embryophyta: Trachcophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROFEINS ADE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: PLAYS A FUNDAMENTAL ROLF IN MICROTUBULE-ORGANIZING
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Caryophyllidue; Caryophyllales, Cheropodiaceae, Alriplex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 24; DB 1; Length 165; 100.0%; Pred. No. 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0: Indels
                                             16-0CT-2001 (Rel. 40, Last sequence update)
15-JMN-2002 (Rel. 41, Last annotation update)
16-JMN-2002 (Rel. 41, Last annotation update)
16-JMN-2002 (ADF).
18-JMN-0R DSN OR SID23.
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01 NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART: SM00102; ADF; 1. PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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InterPro; IPR002108; Actbind_cofin.
Ptam; PF00241; colllin_ADF; I.
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                         16-001-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB 1995 (Rel. 31, Created)
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Hest Local Similarity
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                        NCBI_TaxID-10090;
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O9R0P5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vaccinia virus (strain Copenhagen).
Viruses: dsDNA viruses, no PNA stage; Poxviridae; Chardopoxvirimae;
SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, HELONGS THE CALIRACTIN/CDC31 SUBFAMILY.
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Paoletti E.;
"Appendix to 'The complete DNA sequence of vaccinia virus'.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-91021927; PubMed-2219722;
Goebel S I , Johnson G P , Perkus M.E., Davis S.W., Winslow J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lou.08; Score 24; DB 1; Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3A2D0AC6956HBD6C CRC64;
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EF-IIAND 2 (PROBABLE).
EF-HAND 3 (PROBABLE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE, PS00018, FF_HAND, 4.
Calcium-binding, Repeat, Cell division, Mitosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete DNA sequence of vaccinia virus.";
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01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                     EMBL; M90970; -; NOT_ANNOTATED_CDS. HSSP; P02593; ICDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRI ;
                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002048; EF-hand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19244 MW;
                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00036; ethand; 4.
ProDom; PD000012; EF-hand; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Virology 179:517-563(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82
119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 1
167 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR: 142520; 142520.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHOUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10249;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPLETE GENOME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97 KEELM 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Orthopoxvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KEELM 5
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P21057;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Auregadzia R Y., Ahn B Y., Mass B., Modella B. M. Ahn B Y., Mass B., Modellification, sequence, and expression of the gene encoding a Mr 35,003 subunit of the vaccinia virus DNA dependent ENA polymerase. Y. J. Biol. Chem. 266:13712-13718(1991).

-i. FUNCTION: REQUIRED FOR THE ENVELOPMENT OF INTRACELLULAR NAKED VIRUS AND EGRESS OF EXTRACELLULAR ENVELOPED VIRUS FROM THE CELL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-91259083; PubMed-2045793;
Smith G.L., Chan Y.S., Howard S.T.;
"Nucleotide sequence of 42 kbp of vaccinia virus strain WR from near
the right inverted terminal repeat.";
J. Gen. Virol. 72:1349 1376(1991).
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Virusces, dsDNA virusces, no ENA stage, Poxviridae, Chordopoxvirinae, Orthopoxvirus
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O
                                                                                                                                                                                                                                                                                100.0%; Score 24; DB 1, Length 168; 100 0%; Prod No 55;
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                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                    EXTRACELLULAR

3200B4B0814D2355 CRC64,
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01-MAR-1992 (Rel. 21, Last sequence applate)
01-APR-1993 (Rel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 AA
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EXTRACELLULAR
                                                                                                                                                          SIGNAL-ANCHOR.
                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                           PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MHDLINE=91310644; PubMed=1856205;
InterPro; IPP001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 168 AA; 19555 MW;
                                                                                                                                                                                                              SEQUENCE 168 AA; 19529 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M61187; AAA48331.1; -.
EMBL; A19583; CAA01480.1; ..
PIR; T01770; T01770
                      Pfam; PF00059; lectin_c; 1. SMART; SMO0034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vaccinia virus (strain WR).
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                                                                                                                                                                                                                                                                                                                                              5; Conservative
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168
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168
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A34k OR SALL4R.
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                                                                                                                         Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 KEELM 43
                                                                                                                                                                                                                                                                                                                                                                                                             1 KEELM 5
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P24761:
                                                                                                                                                          TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=India=1967 / Isolate Ind3;
STRAIN=India=1967 / Uselate Ind3;
Shchikhanov S.N., Matchikova S.S., Totmenth A.V., Bilnov V.M.,
Shchikhanov S.N., Matchikova S.S., Totmenth A.V., Bilnov V.M.,
Chichikhan V.E., Garotov V.V., Saffanov P.F., Foolnyakova S.S.,
Shchikhikov V.E., Sardakfachtev E.V., Anjaparides of G., Sandakfachtev L.S.,
Shchikhina E.M., Gashnikov P.V., Anjaparides of G., Sandakfachtev L.S.,
"Creation of a clone library of fragments from the natural variola
virus and study of the structural and functional organization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=India-1967 / Isolate Ind3;
MEDLINE-93202281; PubMcd-8384129;
Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
"Genes of variola and vaccinia viruses necessary to overcome the host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S Lett. 319:80-83(1993).
FUNCTION: FREGUIPED FOF THE ENVELOPMENT OF INTRACELLULAR NAKED
VIRUS AND EGRESS OF EXTRACELLULAR ENVELOPED VIRUS FROM THE CELL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; dsDNA viruses, no RNA stage, Poxviridae, Chordopoxvirinae;
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                                                                                                                                                                                                                                                                                          p33851,
01 FEB 1994 (Re). 28, Created)
01 FFB+1994 (Re). 28, Last sequence update)
01 FEB-1996 (Rel 33, Jast annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     viral genes from a circle of hosts.";
Lokl. Akad Nauk SSSK (2) 402-406(1991)
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SEQUENCE LEW AA; 1961, MW;
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PIR: S46864; S46864.
IntePro: IPP001304; Lectin_C.
Pfam: PP00059; lectin_c; l.
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                                                                         39 KEELM 43
                                                                                                                                                                                                                                                                                                                                                                                                                              Protein A34.
A34R OR A37R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Orthopoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KEELM 5
. 1 KEELM 5
                                                                                                                                                                                                                                                  VA34_VAEV
P33851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                            RESULT 10
VA34_VARV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
                                                                                                                                                                                                                                                                               THE THE WAS COOCCOS OF THE TRANSPORMENT OF THE
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ARBG_ERWCH

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Gaps

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0; Indels

0; Mismatches

Best Local Similarity 100.0 Matches 5; Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTM: PHOSPHORY[ATED AND INACTIVATED BY ARRENCE OR ABSENCE OF PROSPRORYLOWING THE PRESENCE OR ABSENCE OF BETA GLUCOSIDES WHICH AS INDUCERS OF THE OPERON EXPRESSION. ADDITION OF INDUCER PESSION.
                                                                                                                                                                                                                                                                                                                                                                                                    (ARB) OPERON BY FUNCTIONING AS A TRANSCRIPTIONAL ANTITEPMINATOR THIS IS A RNA-RINDING PROTEIN THAT RECOGNIZES A SPECIFIC SEQUENCE LOCATED JUST UPSTREAM OF TWO TERMINATION SITES WITHIN THE OPERON
                                                                                                                                                                                                                                                               el Hassouni M., Henrissat B., Chippaux M., Barras F.; "Nucleotide sequences of the art genes, which control beta-glucoside utilization in Erwicia of the mir "comparison with the Earberichia coli but operon and evidence for a new beta-glycohydrolase family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sales
                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: MEDIATES THE POSITIVE REGULATION OF THE RETA-GLUCOSIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE TRANSCRIPTIONAL ANTITERMINATOR BGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transcription regulation, Activator, RNA binding, Phosphorylation.
SEQUENCE 283 AA: 12826 NW: A589ADROF011A648 CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota: Metacca; Chorduta; Craniata; Vertebrata, Euteicostomi,
Mammalia; Euthoria; Kodentia; Seiurognathi; Muridae; Murinae; Mus.
                                                                                                                                                  Bacteria; Protecharteria: gamma subdivision; Entercharteriarean;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ς:`
                                                                                                                                                                                                                                                                                                                                                including enzymes from eubacteria, archeabacteria, and humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 24; DB 1; Length 283; 190.0%; Prod. No. 93; 0, indels
                              01-MAY-1992 (Bel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P46737; 090025;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSTTE: PS00654; ANTITTERMINATORS_BGLG: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro: IPR001550, BqlG_antitermin.
InterPro: IPP004441; CAT_PRO.
Plam; PF00874; BqlG_antitermin; 2.
                                                                                            Neta-glucoside operon antiterminator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDIJNE-92121114; PubMcd-1732212;
                                                                                                                                                                                                                                                                                                                                                              Hacteriol. 174:765-777(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M81772; AAA24813.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 190.
Matches 5: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAT_RBD;
                                                                                                                                Erwinia chrysanthemi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A42603; A42603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P15401; 1AUG.
                                                                                                                                                                       Pectobacterium.
                                                                                                                                                                                       NCB1_TaxID-556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF03123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260 KEELM 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C6.1A protein.
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ARBG_ERWCH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C61A_MOUSE
                                                                                                              ARHG.
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A Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Arakawa T., Isawa M., Nishi K., Kiyoswa H., Kondo S., Yamanaka I.,
Alisawa K., Isawa M., Nishi K., Kiyoswa H., Kondo S., Yamanaka I.,
Adito T., Exalaka Y., Ashburnor M., Baralov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburnor M., Baralov S., Casavant T.,
A Richischmann W., Gaasterland T., Gissi C., King H., Kochiua H.,
A Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Sakai K., Okido T., Furuno M., Acom H., Baldarelli R., Barsh G.,
Blake J., Boilelli D., Bolunga N., Carninci P., de Bonaldo M.F.,
A Blake J., Boilelli D., Bolunga N., Carninci P., de Bonaldo M.F.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., ice N.H.,
A Yons P., Marchionni L., Maschima J., Manzarcili J., Mombaerts P.,
A Sasaki H., Salo K., Schoenbach C., Seya T., Shibata Y., Solorch K.-F.,
A Wynshaw-Booris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
A Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions and so its content is in no way modified and this statement is not removed. There so the commercial entities requires a license agreement (See http://www.ish-sib.ch/aumonnce/
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                                                                                                                                                              Fisch P., Forster A., Sherrington P.D., Dyer M.J.S., Rabbitts T.H., "The chromosomal translocation t(X:14)(q28:q11) in T-cell pro-
lymphocytic loukacmia breaks within one gene and activates another."; Oncogene 8:3271-3276(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Punctional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82D18B79D8EC5F72 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          K -> R (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCE2_PAT STANDAPD, PRT, 312 AA. P55215: 035399; 01.001.1996 (Rel. 34, Cleated) 15-JUL-1998 (Rel. 36, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21085660; PubMed 11217851;
                                                                                                   IISSUE-Emblyo;
MEDLINE-94067776; PubMed-8247530;
                                                                                                                                                                                                                                                                                                                                                              STRAIN-C57RL/6J; TISSUE-Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; BC021313; AAH21313.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thieppro, Ippnon655; Mov34.
Ptam; PF01398; Mov34; 1.
Probom, PD04392; Mov34.; 1.
SMAEH; SM0232; JAB_MPN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33340 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMB1.; S68022; AAB29006.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291 AA;
                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
NCB1_Tax1D-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280 KEELM 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KEELM 5
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                                                                                                                                                                                                                                                                                                                                 Flaws J.A., Kugu K., Hibovich A.M., Desanti A., Tilly K.; Hirshfield A.N., Tilly J.L.; Interleakin-1 beta-converting enzyme-related protesses (IRDs) and mammalian cell death: dissociation of IRP-induced oligonucleosomal endonuclease activity from morphological apoptosis in granulosa cells of the ovarian follicle.
                                                              Rattus norvegicus (Rat).
Eukarycta: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASKS RESPONSIBLE FOR APOPTOSIS EXECUTION. MIGHT FUNCTION BY ETHER ACTIVATIONS SOME PROPERS PEQUIPED FOR CELL DRAFT OF INACTIVATING SUBUNIT HETERODIMER OF A SMALL AND A LARGE SUBUNIT (BY
                                                                                                                                                                                                   Kaushal G.P., Singh A.B., Shah S.V.;
"Identification of gone family of caspases is rat kideny and altered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIM: THE MATURE PROTEASE CAN PROCESS ITS OWN PROPERTIVE, HUT NOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIR (BY SIMILARITY)
                Caspase-2 precursor (EC 3 4 22 -) (GASP 2) (ICH-1 professe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P13 (BY
F12 (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218A0746212F9646 016064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THAT OF OTHER CASPASES (BY SIMILARITY).
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
SIMILARITY: CONTAINS 1 CAPD DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CASPASE-2 SURINIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CASPASE-2 SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CASPASE-2 SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         April 18 st Tynogen
15-IUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                   expression in ischemia-reperfusion injury.";
Am : Physiol 274:P887-P598(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                       TISSUE=Ovary;
MEDLINE-96042508; PubMed-7588240;
                                                                                                                                                                                   MEDLINE=98191309; Pubmed=9530276;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Endocrinology 136:5842-5053(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50209; CARD; 1.
PROSITE; PS50208; CASPASE_P20; 1.
PROSITE; PS01122; CASPASE_CYS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01121: CASPASP_HIS: 1
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                                                                                                                                                                                                                                                                                     SEQUENCE OF 131-312 FROM N.A.
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InterPro; IPR001309; ICE_p20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; (134684; AACS2260 1; -
HSSP; P29466; lice.
                                                                                                                                                 SEQUENCE OF 1-257 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Piam; PF00619; CARD; 1.—Pram; PF00655; ICE_P10; 1.
Pfam; PF00656; ICE_P20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; (PR001315; CARD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thio: protesse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00114; CARD; 1. SMART; SM00115; CASc; 1.
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253
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                                                                                                                                                                   [ISSUE-Kidney cortex;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312 AA;
                                                                                                              NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEROPS; C14.006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY)
                                                   CASP2 OR ICHI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          - i - FUNCTION
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NON_TER
                                (Fragment)
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SEQUENCE
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECUTION THAN IN A. (ISOFORM 2), AND CHROMOSOMAL THANSLOCATION. MEDLINE 9406-7776; PubMed-8247530; Fisch P., Forster A., Shortington P.D., Dyer M.J.S., Rabbitts T.H.; Fisch Chromosomal translocation t(X:14)(928-941) in T cell prolymphocytic leukaemia breaks within one gene and activates another.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        produced by alternative splicing.
IISSUE SPECIFICITY: Heart, brain, placenta, lung, liver, skeletal
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           Kenwlick S., Levinson B., Taylor S., Shapiro A., Gitschier J., "Isolation and sequence of two genes associated with a CpG island 5'
                                                                                                                                                                                                                                                                                Homo sapiens (Human).
1989/1924a, Metabea, Chifata, Cinnata, Vertebrata, Luteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Propom, PROATA A. May34_1; 1.
SMARP: SM09232; JAB_MPN; 1.
Proto oneOgene, Chromosomal translocation; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (APP-2001) to the EMBL/GenBank/DDBJ databases. 
 -i- ALTERNATIVE PRODUCTS: 2 isotoims: 1 and 2 (shown here); are
                                     ö
190.0%, Score 24, DB 1, Length 312;
190.0%; Pred. No. 1e+02;
ive 0, Mismatches 0; Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISSING (IN ISOFORM 1).
G +5 W (IN REF. 2).
572035801AAF3421 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE PSMD7/C6.1A FAMILY.
                                                                                                                                                                      0, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PMM1: S68015: AAH2905.2; ALILINII.
PMM1: HC00259: AAH2999.1; --
EMM1: HC005540: AAH06540.1; --
INIHELES, EPPN00555; MAV34
                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Placenta;
MPD1/NF-91265009; PubMed-1303175;
                                                                                                                                                                                                                                                                                                                                                                                                                                    of the factor VIII gene.";
Hum Mol Genet 1:179-186(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECON MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oncogene 8:3271-3276(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X64643; CAA45917.1;
                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plam; PF01398; Mov34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 225
316 AA:
                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                  NCB1_1ax1D=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
                                                                                             283 KEELM 287
                                                                                                                                                                                                                                                   C6.1A protein.
C6.1A.
                                                                 1 KEELM 5
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      Cuery Match
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                                Matches
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MEDLINE-9637999; PubMed-8688087;
Built C.J., White O., Olsen G. J., Zhou L., Fleischmann R.D.,
Sutton G.G. Blake J.A., Flizderald L.M., Clayton R.A., Gocayne J.D.,
Korlavage A.R., Dougherry H.A., Tomb J.-F., Adams M.D., Prich C.J.,
OVERDECK R. K., KIKKNESS F.F., Weinsteck K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S., Weinsteck K.G., Merrick J.M., Glodek A.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B. P. Borrdovsky M.,
Klenk H.-P., Fraser C.M., Smith H. O., Wosse G.R., Venter J.C.;
Complete genome sequence of the methanogenic archaeon, Methanococus
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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C
100.0%; Score 24; DB 1; Length 316;
lun n*; Pred No 10+02;
lve 0; Mismatches 0; Indels
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Plam; PF01458; UPF0051; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 316 AA; 35021 MW; 3657AC25CBE473D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        Archaea; Buryarchaeota; Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                jannaschii.";
Science 273:1058-1073(1996).
-!- SIMILARITY: BELONGS TO THE UPF0051 (YCF24) FAMILY.
                                                                                                                                                                                                                                                              01-NnV-1997 (Rel. 35, Created)
01-NnV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                            PRT; 316 AA.
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                                                                                                                                                                                                                                                                                                                              Hypothetical protein MJ0034.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U67462; AAB98015.1; -.
                   Best Local Similarity | 100 C
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-2190;
                                                                                                      305 KEELM 309
                                                                              1 KEELM 5
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  Ouery Match
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